

# SEQUENCE LISTING

<110> MCGILL UNIVERSITY  
GAGNON, Martin  
SARAGOVIC, H. Uri

<120> LIGANDS OF GANGLIOSIDE GD2 AND USES THEREOF

<130> 4810-70826-01

<140> US 10/528,542

<141> 2003-09-19

<150> US 60/412,492

<151> 2002-09-20

<160> 23

<170> PatentIn version 3.2

<210> 1

<211> 13

<212> PRT

<213> Artificial

<220>

<223> GD2 Ligand

<220>

<221> MISC\_FEATURE

<222> (1)..(1)

<223> Xaa = Absent or Tyr or an analogue thereof.

<220>

<221> MOD\_RES

<222> (1)..(1)

<223> The N-terminal group may be of the formula H<sub>2</sub>N-, RHN-, or, RRN-, wherein R at each occurrence is independently selected from (C1-C6) alkyl, (C1-C6) alkenyl, (C1-C6) alkynyl, substituted (C1-C6) alkyl, substituted (C1-C6) alkenyl, or substituted (C1-C6) alkynyl.

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<221> MISC\_FEATURE

<222> (2)..(2)

<223> Xaa = Absent or Cys or an analogue thereof.

<220>

<221> MISC\_FEATURE

<222> (3)..(3)

<223> Xaa = Gly or Tyr or an analogue thereof.

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<221> MISC\_FEATURE

<222> (4)..(4)

<223> Xaa = Gly or Cys or Tyr or an analogue thereof.

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<223> Xaa = Ile or Cys or an analogue thereof.

<220>
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<222> (6)..(6)
<223> Xaa = Thr or Ala or an analogue thereof.

<220>
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<222> (7)..(7)
<223> Xaa = Asn or an analogue thereof.

<220>
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<222> (8)..(8)
<223> Xaa = Tyr or an analogue thereof.

<220>
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<222> (9)..(9)
<223> Xaa = Asn or Gly or an analogue thereof.

<220>
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<222> (10)..(10)
<223> Xaa = Ser or Cys or Val or Thr or an analogue thereof.

<220>
<221> MISC_FEATURE
<222> (11)..(11)
<223> Xaa = Ala or Cys or Tyr or His or Ser or an analogue thereof.

<220>
<221> MISC_FEATURE
<222> (12)..(12)
<223> Xaa = absent or Leu or Cys or Tyr or an analogue thereof.

<220>
<221> MISC_FEATURE
<222> (13)..(13)
<223> Xaa = absent or Met or Tyr or an analogue thereof.

<220>
<221> MOD_RES
<222> (13)..(13)
<223> C-terminal grp is of the formula -C(O)OH, -C(O)R, -C(O)OR,
-C(O)NHR, -C(O)NRR; wherein each R is independently selected from
(C1-C6) alkyl, (C1-C6) alkenyl, (C1-C6) alkynyl, substituted (C1-C6)
alkyl, substituted (C1-C6) alkenyl, or substituted (C1-C6) alkynyl.

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1 5 10

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 <223> Xaa = Absent or Cys or an analogue thereof.  
  
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<223> Xaa = Ser or Cys or Val or Thr or an analogue thereof.

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<222> (13)..(13)

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Gly Gly Ile Ala Asn Tyr Asn Thr Ser  
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<223> Spanning sequence for peptide analogs that actively inhibit  
GD2-mAb 3F8 interactions.

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Ile Thr Asn Tyr Asn  
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GD2-mAb 3F8 interactions.

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<223> Peptide is cyclic.

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<220>  
<223> Peptide Mimic

<220>  
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<222> (1)..(9)  
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1 5

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<210> 22  
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<220>  
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<213> Homo sapiens

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Ile Asn Leu Ile Leu Leu Gly Ser Met Ile Lys Pro Ser Glu Cys Gln  
20 25 30

Leu Glu Val Thr Thr Glu Arg Val Gln Arg Gln Ser Val Glu Glu Glu  
35 40 45

Gly Gly Ile Ala Asn Tyr Asn Thr Ser Ser Lys Glu Gln Pro Val Val  
50 55 60

Phe Asn His Val Tyr Asn Ile Asn Val Pro Leu Asp Asn Leu Cys Ser  
65 70 75 80

Ser Gly Leu Glu Ala Ser Ala Glu Gln Glu Val Ser Ala Glu Asp Glu  
85 90 95

Thr	Leu	Ala	Glu	Tyr	Met	Gly	Gln	Thr	Ser	Asp	His	Glu	Ser	Gln	Val	100	105	110
Thr	Phe	Thr	His	Arg	Ile	Asn	Phe	Pro	Lys	Lys	Ala	Cys	Pro	Cys	Ala	115	120	125
Ser	Ser	Ala	Gln	Val	Leu	Gln	Glu	Leu	Leu	Ser	Arg	Ile	Glu	Met	Leu	130	135	140
Glu	Arg	Glu	Val	Ser	Val	Leu	Arg	Asp	Gln	Cys	Asn	Ala	Asn	Cys	Cys	145	150	155
Gln	Glu	Ser	Ala	Ala	Thr	Gly	Gln	Leu	Asp	Tyr	Ile	Pro	His	Cys	Ser	165	170	175
Gly	His	Gly	Asn	Phe	Ser	Phe	Glu	Ser	Cys	Gly	Cys	Ile	Cys	Asn	Glu	180	185	190
Gly	Trp	Phe	Gly	Lys	Asn	Cys	Ser	Glu	Pro	Tyr	Cys	Pro	Leu	Gly	Cys	195	200	205
Ser	Ser	Arg	Gly	Val	Cys	Val	Asp	Gly	Gln	Cys	Ile	Cys	Asp	Ser	Glu	210	215	220
Tyr	Ser	Gly	Asp	Asp	Cys	Ser	Glu	Leu	Arg	Cys	Pro	Thr	Asp	Cys	Ser	225	230	235
Ser	Arg	Gly	Leu	Cys	Val	Asp	Gly	Glu	Cys	Val	Cys	Glu	Glu	Pro	Tyr	245	250	255
Thr	Gly	Glu	Asp	Cys	Arg	Glu	Leu	Arg	Cys	Pro	Gly	Asp	Cys	Ser	Gly	260	265	270
Lys	Gly	Arg	Cys	Ala	Asn	Gly	Thr	Cys	Leu	Cys	Glu	Glu	Gly	Tyr	Val	275	280	285
Gly	Glu	Asp	Cys	Gly	Gln	Arg	Gln	Cys	Leu	Asn	Ala	Cys	Ser	Gly	Arg	290	295	300
Gly	Gln	Cys	Glu	Glu	Gly	Leu	Cys	Val	Cys	Glu	Glu	Gly	Tyr	Gln	Gly	305	310	315
Pro	Asp	Cys	Ser	Ala	Val	Ala	Pro	Pro	Glu	Asp	Leu	Arg	Val	Ala	Gly	325	330	335
Ile	Ser	Asp	Arg	Ser	Ile	Glu	Leu	Glu	Trp	Asp	Gly	Pro	Met	Ala	Val	340	345	350
Thr	Glu	Tyr	Val	Ile	Ser	Tyr	Gln	Pro	Thr	Ala	Leu	Gly	Gly	Leu	Gln	355	360	365
Leu	Gln	Gln	Arg	Val	Pro	Gly	Asp	Trp	Ser	Gly	Val	Thr	Ile	Thr	Glu	370	375	380
Leu	Glu	Pro	Gly	Leu	Thr	Tyr	Asn	Ile	Ser	Val	Tyr	Ala	Val	Ile	Ser	385	390	395
																		400

Asn Ile Leu Ser Leu Pro Ile Thr Ala Lys Val Ala Thr His Leu Ser  
 405 410 415  
 Thr Pro Gln Gly Leu Gln Phe Lys Thr Ile Thr Glu Thr Thr Val Glu  
 420 425 430  
 Val Gln Trp Glu Pro Phe Ser Phe Ser Phe Asp Gly Trp Glu Ile Ser  
 435 440 445  
 Phe Ile Pro Lys Asn Asn Glu Gly Gly Val Ile Ala Gln Val Pro Ser  
 450 455 460  
 Asp Val Thr Ser Phe Asn Gln Thr Gly Leu Lys Pro Gly Glu Glu Tyr  
 465 470 475 480  
 Ile Val Asn Val Val Ala Leu Lys Glu Gln Ala Arg Ser Pro Pro Thr  
 485 490 495  
 Ser Ala Ser Val Ser Thr Val Ile Asp Gly Pro Thr Gln Ile Leu Val  
 500 505 510  
 Arg Asp Val Ser Asp Thr Val Ala Phe Val Glu Trp Ile Pro Pro Arg  
 515 520 525  
 Ala Lys Val Asp Phe Ile Leu Leu Lys Tyr Gly Leu Val Gly Gly Glu  
 530 535 540  
 Gly Gly Arg Thr Thr Phe Arg Leu Gln Pro Pro Leu Ser Gln Tyr Ser  
 545 550 555 560  
 Val Gln Ala Leu Arg Pro Gly Ser Arg Tyr Glu Val Ser Val Ser Ala  
 565 570 575  
 Val Arg Gly Thr Asn Glu Ser Asp Ser Ala Thr Thr Gln Phe Thr Thr  
 580 585 590  
 Glu Ile Asp Ala Pro Lys Asn Leu Arg Val Gly Ser Arg Thr Ala Thr  
 595 600 605  
 Ser Leu Asp Leu Glu Trp Asp Asn Ser Glu Ala Glu Val Gln Glu Tyr  
 610 615 620  
 Lys Val Val Tyr Ser Thr Leu Ala Gly Glu Gln Tyr His Glu Val Leu  
 625 630 635 640  
 Val Pro Arg Gly Ile Gly Pro Thr Thr Arg Ala Thr Leu Thr Asp Leu  
 645 650 655  
 Val Pro Gly Thr Glu Tyr Gly Val Gly Ile Ser Ala Val Met Asn Ser  
 660 665 670  
 Gln Gln Ser Val Pro Ala Thr Met Asn Ala Arg Thr Glu Leu Asp Ser  
 675 680 685  
 Pro Arg Asp Leu Met Val Thr Ala Ser Ser Glu Thr Ser Ile Ser Leu  
 690 695 700

Ile	Trp	Thr	Lys	Ala	Ser	Gly	Pro	Ile	Asp	His	Tyr	Arg	Ile	Thr	Phe	705	710	715	720
Thr	Pro	Ser	Ser	Gly	Ile	Ala	Ser	Glu	Val	Thr	Val	Pro	Lys	Asp	Arg	725	730	735	
Thr	Ser	Tyr	Thr	Leu	Thr	Asp	Leu	Glu	Pro	Gly	Ala	Glu	Tyr	Ile	Ile	740	745	750	
Ser	Val	Thr	Ala	Glu	Arg	Gly	Arg	Gln	Gln	Ser	Leu	Glu	Ser	Thr	Val	755	760	765	
Asp	Ala	Phe	Thr	Gly	Phe	Arg	Pro	Ile	Ser	His	Leu	His	Phe	Ser	His	770	775	780	
Val	Thr	Ser	Ser	Ser	Val	Asn	Ile	Thr	Trp	Ser	Asp	Pro	Ser	Pro	Pro	785	790	795	800
Ala	Asp	Arg	Leu	Ile	Leu	Asn	Tyr	Ser	Pro	Arg	Asp	Glu	Glu	Glu	Glu	805	810	815	
Met	Met	Glu	Val	Ser	Leu	Asp	Ala	Thr	Lys	Arg	His	Ala	Val	Leu	Met	820	825	830	
Gly	Leu	Gln	Pro	Ala	Thr	Glu	Tyr	Ile	Val	Asn	Leu	Val	Ala	Val	His	835	840	845	
Gly	Thr	Val	Thr	Ser	Glu	Pro	Ile	Val	Gly	Ser	Ile	Thr	Thr	Gly	Ile	850	855	860	
Asp	Pro	Pro	Lys	Asp	Ile	Thr	Ile	Ser	Asn	Val	Thr	Lys	Asp	Ser	Val	865	870	875	880
Met	Val	Ser	Trp	Ser	Pro	Pro	Val	Ala	Ser	Phe	Asp	Tyr	Tyr	Arg	Val	885	890	895	
Ser	Tyr	Arg	Pro	Thr	Gln	Val	Gly	Arg	Leu	Asp	Ser	Ser	Val	Val	Pro	900	905	910	
Asn	Thr	Val	Thr	Glu	Phe	Thr	Ile	Thr	Arg	Leu	Asn	Pro	Ala	Thr	Glu	915	920	925	
Tyr	Glu	Ile	Ser	Leu	Asn	Ser	Val	Arg	Gly	Arg	Glu	Glu	Ser	Glu	Arg	930	935	940	
Ile	Cys	Thr	Leu	Val	His	Thr	Ala	Met	Asp	Asn	Pro	Val	Asp	Leu	Ile	945	950	955	960
Ala	Thr	Asn	Ile	Thr	Pro	Thr	Glu	Ala	Leu	Leu	Gln	Trp	Lys	Ala	Pro	965	970	975	
Val	Gly	Glu	Val	Glu	Asn	Tyr	Val	Ile	Val	Leu	Thr	His	Phe	Ala	Val	980	985	990	
Ala	Gly	Glu	Thr	Ile	Leu	Val	Asp	Gly	Val	Ser	Glu	Glu	Phe	Arg	Leu	995	1000	1005	

Val Asp	Leu Leu Pro Ser	Thr	His Tyr Thr Ala	Thr	Met Tyr Ala
1010		1015		1020	
Thr Asn	Gly Pro Leu Thr	Ser	Gly Thr Ile Ser	Thr	Asn Phe Ser
1025		1030		1035	
Thr Leu	Leu Asp Pro Pro	Ala	Asn Leu Thr Ala	Ser	Glu Val Thr
1040		1045		1050	
Arg Gln	Ser Ala Leu Ile	Ser	Trp Gln Pro Pro	Arg	Ala Glu Ile
1055		1060		1065	
Glu Asn	Tyr Val Leu Thr	Tyr	Lys Ser Thr Asp	Gly	Ser Arg Lys
1070		1075		1080	
Glu Leu	Ile Val Asp Ala	Glu	Asp Thr Trp Ile	Arg	Leu Glu Gly
1085		1090		1095	
Leu Leu	Glu Asn Thr Asp	Tyr	Thr Val Leu Leu	Gln	Ala Ala Gln
1100		1105		1110	
Asp Thr	Thr Trp Ser Ser	Ile	Thr Ser Thr Ala	Phe	Thr Thr Gly
1115		1120		1125	
Gly Arg	Val Phe Pro His	Pro	Gln Asp Cys Ala	Gln	His Leu Met
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Asn Gly	Asp Thr Leu Ser	Gly	Val Tyr Pro Ile	Phe	Leu Asn Gly
1145		1150		1155	
Glu Leu	Ser Gln Lys Leu	Gln	Val Tyr Cys Asp	Met	Thr Thr Asp
1160		1165		1170	
Gly Gly	Gly Trp Ile Val	Phe	Gln Arg Arg Gln	Asn	Gly Gln Thr
1175		1180		1185	
Asp Phe	Phe Arg Lys Trp	Ala	Asp Tyr Arg Val	Gly	Phe Gly Asn
1190		1195		1200	
Val Glu	Asp Glu Phe Trp	Leu	Gly Leu Asp Asn	Ile	His Arg Ile
1205		1210		1215	
Thr Ser	Gln Gly Arg Tyr	Glu	Leu Arg Val Asp	Met	Arg Asp Gly
1220		1225		1230	
Gln Glu	Ala Ala Phe Ala	Ser	Tyr Asp Arg Phe	Ser	Val Glu Asp
1235		1240		1245	
Ser Arg	Asn Leu Tyr Lys	Leu	Arg Ile Gly Ser	Tyr	Asn Gly Thr
1250		1255		1260	
Ala Gly	Asp Ser Leu Ser	Tyr	His Gln Gly Arg	Pro	Phe Ser Thr
1265		1270		1275	
Glu Asp	Arg Asp Asn Asp	Val	Ala Val Thr Asn	Cys	Ala Met Ser
1280		1285		1290	

Tyr	Lys	Gly	Ala	Trp	Trp	Tyr	Lys	Asn	Cys	His	Arg	Thr	Asn	Leu
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Lys	Met	Arg	Pro	Tyr	Asn	His	Arg	Leu	Met	Ala	Gly	Arg	Lys	Arg
	1340					1345					1350			
Gln	Ser	Leu	Gln	Phe										
	1355													